RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/114,844*

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
1                               SEQUENCE LISTING
2
3    (1)    General Information:
4
5      (i) APPLICANT: Ashkenazi, Avi J.
6                     Gurney, Austin
7
8     (ii) TITLE OF INVENTION: RTD Receptor
9
10   (iii) NUMBER OF SEQUENCES: 5
11
12    (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Genentech, Inc.
14           (B) STREET: 1 DNA Way
15           (C) CITY: South San Francisco
16           (D) STATE: California
17           (E) COUNTRY: USA
18           (F) ZIP: 94080
19
20     (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: WinPatin (Genentech)
25
26    (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER:
28           (B) FILING DATE: 14-Jul-1998
29           (C) CLASSIFICATION:
30
31   (vii) PRIOR APPLICATION DATA:
32           (A) APPLICATION NUMBER: 60/056974
33           (B) FILING DATE: 26-AUG-1997
34
35  (viii) ATTORNEY/AGENT INFORMATION:
36           (A) NAME: Marschang, Diane L.
37           (B) REGISTRATION NUMBER: 35,600
38           (C) REFERENCE/DOCKET NUMBER: P1129R1
39
40    (ix) TELECOMMUNICATION INFORMATION:
41           (A) TELEPHONE: 650/225-5416
42           (B) TELEFAX: 650/952-9881
43  (2) INFORMATION FOR SEQ ID NO:1:
44
45     (i) SEQUENCE CHARACTERISTICS:
46           (A) LENGTH: 386 amino acids
```

ENTERED

```
47          (B) TYPE: Amino Acid
48          (D) TOPOLOGY: Linear
49
50     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
51
52   Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
53    1               5                  10                  15
54
55   Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
56                   20                  25                  30
57
58   Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
59                   35                  40                  45
60
61   Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
62                   50                  55                  60
63
64   Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
65                   65                  70                  75
66
67   Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
68                   80                  85                  90
69
70   Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
71                   95                 100                 105
72
73   Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
74                  110                 115                 120
75
76   Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
77                  125                 130                 135
78
79   Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
80                  140                 145                 150
81
82   Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
83                  155                 160                 165
84
85   Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
86                  170                 175                 180
87
88   Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
89                  185                 190                 195
90
91   Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
92                  200                 205                 210
93
94   His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
95                  215                 220                 225
96
97   Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
98                  230                 235                 240
99
```

INPUT SET: S27566.raw

```
100    Lys Gly Ile Cys Ser Gly Gly Gly Gly Pro Glu Arg Val His
101                245                 250                 255
102
103    Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
104                260                 265                 270
105
106    Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
107                275                 280                 285
108
109    Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
110                290                 295                 300
111
112    Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
113                305                 310                 315
114
115    Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
116                320                 325                 330
117
118    Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
119                335                 340                 345
120
121    Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
122                350                 355                 360
123
124    Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
125                365                 370                 375
126
127    Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
128                380                 385 386
129
130    (2) INFORMATION FOR SEQ ID NO:2:
131
132       (i) SEQUENCE CHARACTERISTICS:
133           (A) LENGTH: 2082 base pairs
134           (B) TYPE: Nucleic Acid
135           (C) STRANDEDNESS: Single
136           (D) TOPOLOGY: Linear
137
138      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
139
140
141    CCAACTGCAC CTCGGTTCTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG 50
142
143    ATCCCTCGAC CTCGACCCAC GCGTCCGGAA CCTTTGCACG CGCACAAACT 100
144
145    ACGGGGACGA TTTCTGATTG ATTTTTGGCG CTTTCGATCC ACCCTCCTCC 150
146
147    CTTCTC  ATG GGA CTT TGG GGA CAA AGC GTC CCG ACC GCC 189
148            Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
149             1               5                   10
150
151    TCG AGC GCT CGA GCA GGG CGC TAT CCA GGA GCC AGG ACA 228
152    Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
```

```
153                15                        20
154
155    GCG TCG GGA ACC AGA CCA TGG CTC CTG GAC CCC AAG ATC 267
156    Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
157     25                 30                        35
158
159    CTT AAG TTC GTC GTC TTC ATC GTC GCG GTT CTG CTG CCG 306
160    Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
161         40                     45                    50
162
163    GTC CGG GTT GAC TCT GCC ACC ATC CCC CGG CAG GAC GAA 345
164    Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu
165                 55                     60
166
167    GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG AGG CGC 384
168    Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
169.         65                     70                    75
170
171    AGC CTC AAG GAG GAG GAG TGT CCA GCA GGA TCT CAT AGA 423
172    Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
173                 80                     85
174
175    TCA GAA TAT ACT GGA GCC TGT AAC CCG TGC ACA GAG GGT 462
176    Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
177     90                     95                   100
178
179    GTG GAT TAC ACC ATT GCT TCC AAC AAT TTG CCT TCT TGC 501
180    Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys
181         105                    110                   115
182
183    CTG CTA TGT ACA GTT TGT AAA TCA GGT CAA ACA AAT AAA 540
184    Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys
185                 120                    125
186
187    AGT TCC TGT ACC ACG ACC AGA GAC ACC GTG TGT CAG TGT 579
188    Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys
189         130                    135                   140
190
191    GAA AAA GGA AGC TTC CAG GAT AAA AAC TCC CCT GAG ATG 618
192    Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met
193         145                    150
194
195    TGC CGG ACG TGT AGA ACA GGG TGT CCC AGA GGG ATG GTC 657
196    Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val
197     155                    160                   165
198
199    AAG GTC AGT AAT TGT ACG CCC CGG AGT GAC ATC AAG TGC 696
200    Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
201         170                    175                   180
202
203    AAA AAT GAA TCA GCT GCC AGT TCC ACT GGG AAA ACC CCA 735
204    Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro
205                 185                    190
```

```
206
207   GCA GCG GAG GAG ACA GTG ACC ACC ATC CTG GGG ATG CTT 774
208   Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu
209       195             200             205
210
211   GCC TCT CCC TAT CAC TAC CTT ATC ATC ATA GTG GTT TTA 813
212   Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu
213           210             215
214
215   GTC ATC ATT TTA GCT GTG GTT GTG GTT GGC TTT TCA TGT 852
216   Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys
217   220             225             230
218
219   CGG AAG AAA TTC ATT TCT TAC CTC AAA GGC ATC TGC TCA 891
220   Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser
221       235             240             245
222
223   GGT GGT GGA GGA GGT CCC GAA CGT GTG CAC AGA GTC CTT 930
224   Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu
225           250             255
226
227   TTC CGG CGG CGT TCA TGT CCT TCA CGA GTT CCT GGG GCG 969
228   Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
229       260             265             270
230
231   GAG GAC AAT GCC CGC AAC GAG ACC CTG AGT AAC AGA TAC 1008
232   Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
233           275             280
234
235   TTG CAG CCC ACC CAG GTC TCT GAG CAG GAA ATC CAA GGT 1047
236   Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
237   285             290             295
238
239   CAG GAG CTG GCA GAG CTA ACA GGT GTG ACT GTA GAG TYG 1086
240   Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
241       300             305             310
242
243   CCA GAG GAG CCA CAG CGT CTG CTG GAA CAG GCA GAA GCT 1125
244   Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
245           315             320
246
247   GAA GGG TGT CAG AGG AGG AGG CTG CTG GTT CCA GTG AAT 1164
248   Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
249       325             330             335
250
251   GAC GCT GAC TCC GCT GAC ATC AGC ACC TTG CTG GAT GCC 1203
252   Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
253           340             345
254
255   TCG GCA ACA CTG GAA GAA GGA CAT GCA AAG GAA ACA ATT 1242
256   Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
257   350             355             360
258
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/114,844*

INPUT SET: S27566.raw

Line   Error   Original Text